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GPU-based 3D iceball modelling for fast cryoablation simulation and planning

IJCARS / MICCAI 2018 invited paper

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Abstract *Purpose* The elimination of abdominal tumors by percutaneous cryoablation has been shown to be an effective and less invasive alternative to open surgery. Cryoablation destroys malignant cells by freezing them with one or more cryoprobes inserted into the tumor through the skin. Alternating cycles of freezing and thawing produce an enveloping iceball that causes the tumor necrosis. Planning such a procedure is difficult and time-consuming, as it is necessary to plan the number and cryoprobe locations, and predict the iceball shape which is also influenced by the presence of heating sources, e.g., major blood vessels and warm saline solution injected to protect surrounding structures from the cold.

Methods This paper presents a new method for fast GPU-based iceball modeling based on the simulation of thermal propagation in the tissue. Our algorithm solves the heat equation within a cube around the cryoprobes tips and accounts for the presence of heating sources around the iceball.

Results Experimental results of two studies have been obtained: an ex-vivo warm gel setup, and simulation on five retrospective patient cases of kidney tumors cryoablation with various levels of complexity of the vascular structure and warm saline solution around the tumor tissue. The experiments have been conducted in various conditions of cube size and algorithm implementations. Results show that it is possible to obtain an accurate result within seconds.

Conclusion The promising results indicate that our method yields accurate iceball shape predictions in a short time and is suitable for surgical planning.

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Keywords Preoperative planning · cryoablation · iceball modeling · GPU-based heat simulation

1 Introduction

The treatment of abdominal tumors has undergone significant improvements with the introduction of percutaneous procedures based on thermal ablation. The advantages of these minimally invasive procedures is that they lead to faster patient recovery, shorter hospital stays, lower patient morbidity, and fewer, smaller skin scars. Oftentimes, they also preclude total organ removal, preserve most of the treated organ functionality, and enable the treatment of patients that cannot undergo open surgery or organ resection.

Cryoablation is a percutaneous procedure that was first introduced in the 1960s [1]. Cryoablation interventions destroy malignant tumor cells by freezing them with one or more needles, called cryoprobes, inserted into the tumor through the skin under imaging guidance, e.g., CT, MR or ultrasound. Alternating cycles of freezing and thawing by decompressing a gas through the cryoprobes tips produce an enveloping iceball that causes the tumor necrosis [2]. The recommended temperature to achieve destruction of cancerous cells is -50°C to 0°C [3].

The numerous advantages of percutaneous cryoablation have made this procedure very popular in the past two decades. However, the difficulties of planning an optimal position for the cryoprobes and of anticipating the final result is a limitation in many cases [4]. Indeed, to be most effective, cryoablation requires careful preoperative planning of the cryoprobes to be inserted. The goal is to find the number and positions for the cryoprobes that are safe and that produce an optimal iceball shape that covers the entire tumor with an additional margin to ensure its complete ablation. The simulation of the iceball formation and its final shape is required to ensure an effective treatment. However, simulating the iceball generated from multiple cryoprobes while taking into account various factors, i.e., the surrounding anatomy and the injection of protective warm fluid is challenging. In addition, the synergistic effect created by several cryoprobes depends on their actual location and influences the final shape of the iceball [5].

This paper presents a new method for fast and accurate GPU-based iceball modeling based on the simulation of thermal propagation in tissue based on the solution of the heat equation that accounts for the influence of heating sources around the iceball. The paper is organized as follows. We start with a brief review the relevant state of the art. Next, we describe a fast GPU-based method for simulating the cold propagation in tissue from the freezing cryoprobes tips and for modeling the resulting iceball. We then present two experiments that validate our model: an ex-vivo setup with warm gel and five and five retrospective patient cases of kidney tumors cryoablation.

2 State of the Art

The goal of cryoablation is to release an extreme cold from the tip of one or more cryoprobes inserted into a target. The propagation of cold produces an iceball around the cryoprobe tip, which is described in the manufacturer’s booklets as an

ellipsoidal iso-surface of known theoretical dimensions. When several cryoprobes are used, a larger, more complex iceball is produced by a synergistic effect. However, due to the complex characteristics of the human body physiology and the heterogeneity of the anatomical structures surrounding the cryoprobes, the actual iceball may not have the expected theoretical ellipsoid shape and size, and is thus difficult for the surgeon to anticipate. Consequently, the accurate prediction of the iceball growth and final shape is essential to help the clinician to ensure the maximal coverage of the tumor while preventing possible damages to surrounding structures, and to choose the best insertion trajectories for the cryoprobes that will create the desired tumor-enclosing iceball.

Various research groups have proposed methods for computing the iceball shape to assist clinicians in preoperative planning. Butz *et al.* [6] developed one of the first simulations of a cryoablation iceball. In this early work, the iceball is modeled as a 3D ellipsoid forming around the cryoprobe tip without taking into account its surroundings. The iceball model is used in conjunction with a single cryoprobe placement optimization algorithm. Recent works describe advanced mathematical models to accurately simulate the growth and the final shape and size of the iceball in a simple, homogeneous gel surrounding, and in realistic soft tissue conditions. Most of these works base their models on the Pennes heat propagation equation [7]. However, the complexity, numerical sensitivity, and computational cost of this model motivated researchers to develop simplified models, which introduce unknown inaccuracies. Magalov *et al.* [4] describe a simplified model for multiple cryoprobes planning that simulates the iceball growth in an aquasonic clear ultrasonic gel. The shape of the iceball resulting from various cryoprobes is investigated in a laboratory environment. Ge *et al.* [8] incorporate surrounding gel models into the simulation but do not validate their results with real soft tissue properties. In subsequent papers [9,10], the authors describe a model that accounts for the presence of vascular systems during freezing. Nabaei *et al.* [11] investigate the effect of blood vessels adjacent to tumors. Their theoretical study shows that large blood vessels (>4mm diameter) significantly affect the shape of the iceball, as the heat blood flow heat prevents the cold from propagating. Other studies describe advanced models validated in gel [12], or tailored to other organs, e.g., the prostate [13] and the lungs [14,15].

None of the works discussed above focuses on the iceball simulation computation time, which can limit the scope of the preoperative planning by reducing to a handful the scenarios that can be simulated and tested. Indeed, the optimization of cryoprobes placement requires to iterate over many possible candidate cryoprobe configurations and to simulate the iceball at each iteration. Thus, the reduction of the computation time becomes important. Talbot *et al.* [16] describe a GPU-based method to compute the iceball resulting from multiple cryoprobes. Their method significantly decreases the iceball modelling computation time to <30 secs, but does not take into account the surrounding structures.

An alternative to cryoablation is hyperthermia, in which tumor necrosis is induced by extreme heat propagation instead of cold. The most common hyperthermia procedure is radio frequency ablation. As for cryoablation, several groups have investigated the modelling of the isothermal surface to predict the outcome and to evaluate the damages to adjacent structures. Villard *et al.* [17,18] describe a simplified ellipsoidal model that takes into account nearby vascular structures. The influence of blood vessels near the tumor was also investigated in [19]. Advanced

models for cryoablation have also been described in [20,21]. None of these works attempts to reduce the simulation computation time. Rieder *et al.* [22] describe a GPU-based implementation of heat propagation for radio frequency ablation procedures. Their model, which was developed for a single probe, is based on weighted distance fields, and has been simplified to allow real-time computation.

In conclusion, to the best of our knowledge, no model based on a realistic mathematical representation of heat propagation that accounts for the influence of surrounding anatomical structures and that is computationally efficient so it can be used with a probe placement optimization algorithm has been proposed.

3 Materials and Methods

3.1 General formulation

The general formulation of heat equation describes the distribution of heat over time t in a region defined in a Cartesian coordinate system [23]. The spatial propagation of heat in (x, y, z) is described by the partial differential equation:

$$C \frac{\partial T}{\partial t} = \frac{\partial}{\partial x} (K_x \frac{\partial T}{\partial x}) + \frac{\partial}{\partial y} (K_y \frac{\partial T}{\partial y}) + \frac{\partial}{\partial z} (K_z \frac{\partial T}{\partial z}) + I(x, y, z, t) \quad (1)$$

where I is the internal heat generation function, t is time, and constants K and C are the spatial thermal conductivities in x, y, z and the heat capacity, respectively.

This continuous formulation can be approximated by a discretization in which $\Delta x = \Delta y = \Delta z$ is the spacing between a cell (i, j, k) and its neighbours in the x, y, z directions. The discrete formulation approximation is then:

$$T_{i,j,k}^{new} = T_{i,j,k} + \frac{\Delta t \cdot \beta}{C_{i,j,k} (\Delta x)^3} \cdot H_{i,j,k} \quad (2)$$

where $C_{i,j,k}$ is the volumetric heat capacity. The new temperature $T_{i,j,k}^{new}$ after a time step Δt is computed by adding to the previous temperature $T_{i,j,k}$ the heat flow coefficient $H_{i,j,k}$ multiplied by a relaxation factor $\beta \in [1, 2]$ (in our simulations, β was set to 1.95).

In this formulation, the volumetric heat capacity $C_{i,j,k}$ at cell (i, j, k) depends on the current temperature and is defined as:

$$C_{i,j,k} = \begin{cases} c_f & T_{i,j,k} < T_{ml} \\ \frac{c_f}{T_{mu} - T_{ml}} \frac{q_l}{T_{mu} - T_{ml}} + \frac{c_f + c_u}{2}, & T_{ml} \leq T_{i,j,k} \leq T_{mu} \\ c_u & T_{i,j,k} > T_{mu} \end{cases} \quad (3)$$

where c_f and c_u represent the effective thermal capacities of frozen and unfrozen tissue, respectively, q_l is the latent heat when the phase transition occurs, and T_{ml} and T_{mu} are the lower and the upper limits of the phase transition.

The heat flow $H_{i,j,k}$ for cell (i, j, k) is computed from its six neighbours:

$$\begin{aligned} H_{i,j,k} = & \kappa_{i-\frac{1}{2},j,k} \cdot (T_{i-1,j,k} - T_{i,j,k}) + \kappa_{i+\frac{1}{2},j,k} \cdot (T_{i+1,j,k} - T_{i,j,k}) + \\ & \kappa_{i,j-\frac{1}{2},k} \cdot (T_{i,j-1,k} - T_{i,j,k}) + \kappa_{i,j+\frac{1}{2},k} \cdot (T_{i,j+1,k} - T_{i,j,k}) + \\ & \kappa_{i,j,k-\frac{1}{2}} \cdot (T_{i,j,k-1} - T_{i,j,k}) + \kappa_{i,j,k+\frac{1}{2}} \cdot (T_{i,j,k+1} - T_{i,j,k}) \end{aligned} \quad (4)$$

In this equation, $\kappa_{i-\frac{1}{2},j,k}$, $\kappa_{i,j-\frac{1}{2},k}$, $\kappa_{i,j,k-\frac{1}{2}}$ denote the thermal conductances between cell (i, j, k) and the previous adjacent cells in the x, y, z directions, respectively. Similarly, $\kappa_{i+\frac{1}{2},j,k}$, $\kappa_{i,j+\frac{1}{2},k}$, $\kappa_{i,j,k+\frac{1}{2}}$ denote the conductances between cell (i, j, k) and posterior adjacent cells, as in [23]. The thermal conductance $\kappa_{i,j,k+\frac{1}{2}}$ is defined as:

$$\kappa_{i,j,k+\frac{1}{2}} = \frac{\Delta x}{1/(2K_{i,j,k}) + 1/(2K_{i,j,k+1}) + R_{i,j,k+\frac{1}{2}}} \quad (5)$$

where $K_{i,j,k}$ and $K_{i,j,k+1}$ are the thermal conductivities of the current cell (i, j, k) and its adjacent cell $(i, j, k+1)$. The five κ values in Eq. (3) are defined similarly. The thermal resistance between these cells is denoted by $R_{i,j,k+\frac{1}{2}}$. Since the thermal resistance has a very small impact on heating flows, it is neglected in the rest of this paper.

The thermal conductivity $K_{i,j,k}$ of a cell (i, j, k) is defined as:

$$K_{i,j,k} = \begin{cases} K_f & T_{i,j,k} < T_{ml} \\ \frac{K_f + K_u}{2} & T_{ml} \leq T_{i,j,k} \leq T_{mu} \\ K_u & T_{i,j,k} > T_{mu} \end{cases} \quad (6)$$

where K_f and K_u are the effective thermal conductivities for frozen and unfrozen tissue, respectively.

To avoid numerical instability in the heat transform equation, the time step Δt is set to 0.05 secs, which satisfies the stability criterion:

$$\Delta t < \frac{C_{i,j,k}(\Delta x)^3}{\Sigma \kappa}, \forall i, j, k \quad (7)$$

where

$$\Sigma \kappa = \kappa_{i-\frac{1}{2},j,k} + \kappa_{i+\frac{1}{2},j,k} + \kappa_{i,j-\frac{1}{2},k} + \kappa_{i,j+\frac{1}{2},k} + \kappa_{i,j,k-\frac{1}{2}} + \kappa_{i,j,k+\frac{1}{2}} \quad (8)$$

To simulate the growth of the iceball using this formulation, the 3D heat propagation is computed iteratively within a cubic grid of voxels centered at the cryoprobe tip, or at the centroid of the tips when several cryoprobes are used. To obtain a high accuracy, a very fine grid can be used, but at the cost of efficiency. In this study, we use a grid resolution of $\Delta x = \Delta y = \Delta z = 1$ mm, which is smaller than the diameter of the thinnest cryoprobe used in the procedures (*IceRod* by Galil Medical, diameter 1.5 mm); this value proved to be an appropriate trade-off between accuracy and speed.

In the simulation cube, the voxels located in the active part of the cryoprobes are labeled as the source of cold – their temperature is kept constant during the freezing cycles at the freezing temperature. Similarly, during active thawing cycles, they are kept constant at the active thawing temperature. During passive thawing cycles, the temperature in these voxels is computed as for normal tissue. Boundary conditions are represented by the voxels at the boundaries of the cube, which are set to be to the temperature of the environment.

3.2 Propagation of cold in the human body near heating sources

In the human body, heat is generated by metabolism, mostly from blood perfusion and reactions within the tissue cells. This heat production interferes with the cold propagation coming from the cryoprobes and influences the final size and shape of the iceball. Due to this phenomenon, the iceball growth is slower in-vivo than ex-vivo. To take this into account in the simulation, we add the thermodynamic properties of the human body in the last term of Eq. 1, which represents the internal heat generation:

$$C \frac{\partial T}{\partial t} = \frac{\partial}{\partial x} (K_x \frac{\partial T}{\partial x}) + \frac{\partial}{\partial y} (K_y \frac{\partial T}{\partial y}) + \frac{\partial}{\partial z} (K_z \frac{\partial T}{\partial z}) + C_b \cdot \omega_b(T) \cdot (T_a - T_t) + Q_m \quad (9)$$

where C_b denotes the heat capacity of blood, ω_b is the blood perfusion rate, T_a is the arterial temperature, T_t is the temperature at time t , and Q_m is the metabolic heat rate of tissue.

The blood perfusion rate $\omega_b(T)$ depends on the current temperature and is defined as:

$$\omega_b(T) = \begin{cases} 0 & T_{i,j,k} \leq T_{mu} \\ \omega_b & T_{i,j,k} > T_{mu} \end{cases} \quad (10)$$

The discrete approximation of Eq. 9 is then:

$$T_{i,j,k}^{new} = T_{i,j,k} + \frac{\Delta t \cdot \beta}{C_{i,j,k} (\Delta x)^3} \cdot H_{i,j,k} + C_b \cdot \omega_b(T_{i,j,k}) \cdot (T_a - T_{i,j,k}) + Q_m \quad (11)$$

Another important source of interference with the propagation of cold in the human body is the presence of a major blood vessel or of injected warm protective liquid or gas close to the tumor and the iceball. The presence of these heat sources can significantly impair the normal propagation of cold and thus change the final shape of the iceball. To model this phenomenon, the voxels of the cube that corresponds to these structures are labeled, and their temperature is kept constant and equal to the source temperature during the entire simulation. In this paper, we assume that all sources of heat are constant and homogeneous.

3.3 Validation in-silico

We first validated the results of our model and simulation with an in-silico study using gel properties. The goal was to measure the performance of our simulation in terms of accuracy and computation times under theoretical conditions.

To achieve this goal, we ran various simulations using parameters that reproduced the conditions used in the physical experiment described in [24]. In that paper, the authors used a thermocouple matrix structure that was designed to measure the iceball temperatures in an ultrasound gel at 37°C. To simulate the same conditions, we used the thermophysical properties of a similar gel [25].

Since this experiment uses a gel, there is no internal heat generation. Thus, we use Eq. 1 and omit the last term, $I(x, y, z, t)$. Since the gel was maintained at a

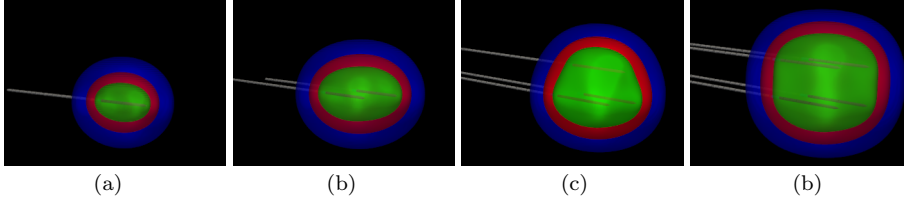


Fig. 1: In-silico validation. Iceball created by one to four (a-d) evenly spaced cryoprobes (gray lines, left to right) arranged in parallel at 20mm intervals. The boundaries of the isothermal surfaces are shown for temperatures of 0°C (blue) -20°C (red) and -40°C (green).

temperature of 37°C from the outside, the boundary conditions were applied with a fixed temperature of 37°C on the external voxels of the cube.

We simulated the propagation of cold with one to four evenly spaced cryoprobes arranged in parallel at 20mm intervals in a cube of $100 \times 100 \times 100 \text{ mm}^3$ (Fig. 1). The experiment was conducted with the specifications of two types of cryoprobes from Galil Medical: *IceEdge* 2.4 mm (10G) and *IceRod* 1.5 mm (17G).

Each experiment simulated three cycles: 10 mins of freezing, followed by 5 mins of passive thaw, followed by 10 mins of freezing. We used the parameters provided by the manufacturer to model the action of the cryoprobes. For *IceEdge*, the freezing temperature at the cryoprobe’s tip was set to -138.0°C , and the length of the active freezing part was set to 28mm starting at 5.2mm from the tip. For *IceRod*, the freezing temperature was set to -119.4°C , the length of the active freezing part was set to 31mm at 4.2mm from the tip.

For all settings, we computed the diameters of the resulting 0°C , -20°C and -40°C isotherm surfaces at their largest sections, perpendicularly to the probe’s axis (Fig. 1). We then compared our simulation results with the dimensions measured in the physical world as reported in [24].

3.4 Validation on intraoperative MRI images

To validate our simulations in human body conditions, we conducted a second experiment using retrospective preoperative and intraoperative MRI scans of actual renal cryoablation procedures. Datasets of five patients were used, with different levels of complexity of the anatomical environment surrounding the tumor: tumor located close to major blood vessels, close to warm saline solution injected to protect sensitive organs nearby from being frozen, or far from heating structures.

The procedure performed by the surgeon differs from that of the gel experiment. The cryoablation process consisted of four cycles: 10 mins of active freezing, followed by 9 mins of passive thawing and 1 min of active thawing, and again 10 mins of active freezing. The active freezing temperature of *IceRod* was set to -119.4°C ; the active thawing temperature was set to 52.0°C . During the cryoablation, a saline solution at 37.0°C was continuously injected around the kidney.

The preoperative and intraoperative MRI scans of all patients have a resolution of $256 \times 232 \times 25$ voxels with a $1.5 \times 1.5 \times 5 \text{ mm}^3$ voxel size. The scans were acquired during the cryoablation procedure at three stages: 1) before cryoablation; 2) after

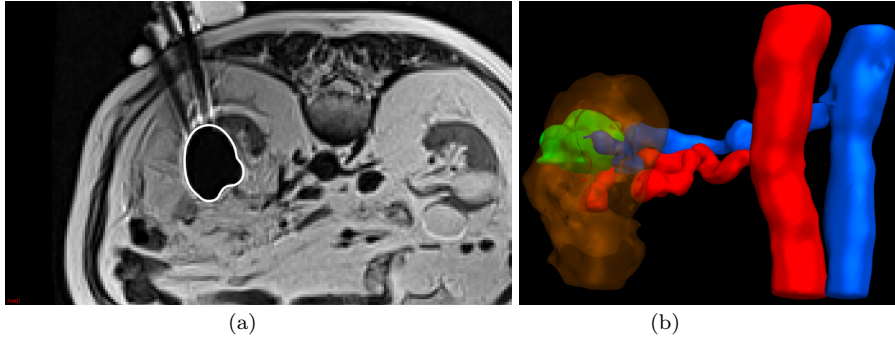


Fig. 2: Intraoperative MRI scan validation. (a): representative MRI slice with the superimposed iceball contour (white); (b): visualization of the structures of interest after segmentation: kidney (brown), tumor (green), artery (red) and vein (blue).

Table 1: Thermophysical properties of biological tissue and blood [8].

Definition	Symbol	Unit	Value
Metabolic heat rate	Q_m	W.m^{-3}	4200
Latent heat	q_l	kJ.kg^{-1}	2500
Upper limit of phase transition	T_{mu}	K	272
Lower limit of phase transition	T_{ml}	K	265
Thermal conductivity of frozen tissue	K_f	$\text{W.m}^{-1}.\text{K}^{-1}$	2.0
Thermal conductivity of unfrozen tissue	K_u	$\text{W.m}^{-1}.\text{K}^{-1}$	0.5
Specific heat of frozen tissue	c_f	$\text{J.kg}^{-1}.\text{K}^{-1}$	1800
Specific heat of unfrozen tissue	c_u	$\text{J.kg}^{-1}.\text{K}^{-1}$	3600
Specific heat of blood	c_b	$\text{J.kg}^{-1}.\text{K}^{-1}$	3850
Blood perfusion rate per unit tissue volume	ω_b	$\text{kg.m}^{-3}.\text{s}^{-1}$	0.29

10 mins of freezing, and; 3) at the end of the cryoablation. In some cases, the segmentation of the structures of interest was particularly challenging due to the injection of saline solution between preoperative and intraoperative images that causes a deformation of the internal organs.

For each patient, we first registered the preoperative and the intraoperative MRI scan using interactive deformable point-based registration. Then, on the registered preoperative MRI scan, we interactively segmented the kidney and the tumor. To obtain the ground-truth models of the structures of interest, we segmented on the intraoperative MRI scan the injected saline solution when it was present, the renal vessels (vein and artery) when they were close to the iceball, and the final iceball after the second freezing cycle. Note that during a cryoablation procedure, the iceball, which corresponds to the 0°C iso-surface, appears clearly as a black hole in the MRI scan (Fig. 2). We also segmented the cryoprobes, and used their positions as an input to reproduce the same setup in our simulations. Both the segmentation and the registration were performed under the supervision of an experienced radiologist. Fig. 2 shows an example of a case.

The simulations were performed with commonly used soft tissue parameters accounting for frozen/unfrozen state [8], summarized in Table 1.

To measure the accuracy of our model and simulation, the Hausdorff distance and the Dice coefficient were computed to compare the similarity of the segmented

and simulated iceball at the end of the process. This shape comparison was performed only for the 0°C iso-surface that corresponds to the iceball shape visible on the MRI image.

3.5 Parallelization

We implemented the method described above in three different setups. The first one is a simple, single-thread version. It consists of a sequential examination of the cube voxels to compute the new temperature at each voxel based on its previous state and those of its neighbours. Two cubes are used to store the temperatures at times $t - 1$ and t .

The second version is a multi-thread version that supports running in parallel several simulations. In this version, the cube is split into layers. The number of layers corresponds to the number of cores available on the computer CPU. Each layer can run independently, as the currently computed temperatures only depend on the previous state, so the different threads are not concurrent. Two matrices contain respectively the previous state and the current state of temperatures in the cube, to avoid concurrency clashes.

The third version has been implemented using the CUDA toolkit for NVidia's GPUs. To optimally use the parallelization capabilities of the GPU processing units and to avoid the repeated computation by two threads on the same heat cell, we also use two matrices to represent the previous and current states.

4 Results

4.1 Validation in-silico

Fig. 3 shows the results of the experiment with the gel parameters. Table 2 summarizes the maximum diameters of the ground truth isothermal surfaces at 0°C , -20°C and -40°C (from [24]) and of the simulated iceballs, for the *IceRod* and the *IceEdge* cryoprobe models.

The results of the simulation are very close to the measurements, with a mean error of 0.28 mm, i.e. 5.8% of the diameter of the reference iceball. Note that the configuration of the multi-cryoprobe thermocouple matrix structure used in [24], which was designed with a minimum spacing of 5mm between the measuring thermocouples, which is a potential source of inaccuracy.

The simulation results were obtained with desktop PC equipped with a core-i7 3.40GHz CPU with 16Gb RAM and a GeForce GTX-1060 GPU with 6GB memory. The mean computation times of the simulation in CPU single thread and GPU implementations were of 540 secs. and 84 secs. respectively for a simulation in a $100 \times 100 \times 100 \text{ mm}^3$ cube. The GPU implementation was on average $\times 6.4$ faster than the CPU implementation.

4.2 Validation on intraoperative MRI

The second experiment was conducted on the datasets of the five patient cases who underwent renal cryoablation. The cases have various characteristics in terms of

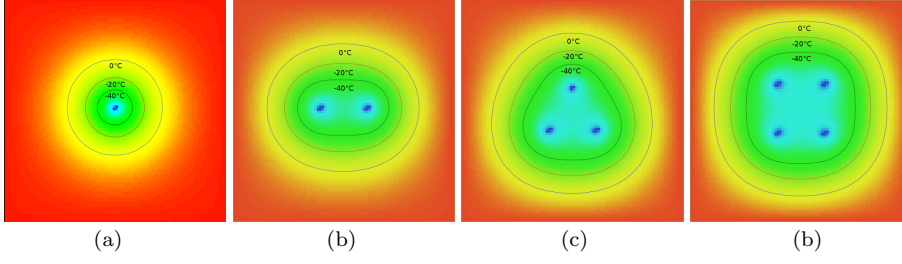


Fig. 3: Heat propagation simulation at the end of the for one to four (a-d) *IceEdge* cryoprobes evenly spaced 20mm apart (left to right). The figures show the largest 2D cross-sections of the iceball in the cryoprobe's axis. The color map is in the range $[-138.0, 37]^{\circ}\text{C}$.

Table 2: Maximum diameters (mm) of ground truth and simulated iceball.

Cryoprobe	# of needles	Ground truth [24]			Simulation		
		0°C	-20°C	-40°C	0°C	-20°C	-40°C
<i>IceEdge</i>	1	43	33	24	40	29	21
	2	62	52	42	61	51	42
	3	69	59	49	64	53	44
	4	75	66	56	71	61	50
<i>IceRod</i>	1	36	26	18	39	27	18
	2	57	47	37	60	48	39
	3	62	52	44	61	50	40
	4	69	59	50	67	57	47

Table 3: Characteristics of the patient cases.

Patient case	Nearby vessels	Saline solution	Number of cryoprobes
1		yes	4
2	yes		4
3	yes		3
4	yes	yes	4
5			5

the location of the tumor with respect to the blood vessel, the use of the dissection saline solution, and the number of cryoprobes as detailed in Table 3.

Simulations were performed for three different cube sizes sizes: small (60 mm), medium (80 mm), and large (100 mm) to evaluate the performance in terms of the computation time *vs.* the results accuracy.

Fig. 4 and 5 show examples of the simulation results. Fig. 4 shows the simulated temperature distribution for cases 2 and 4 in a cube of 80 mm. Note how the presence of the blood vessels and the saline solution significantly influence the iceball shape.

Fig. 5a shows 3D views of the ground truth and simulated iceballs, the four cryoprobes, the blood vessels and the saline solution. Note that the simulated iceball is tightly fit around the blood vessels and is deformed by the saline solution. Fig. 5b shows the simulated iceball and the theoretical ellipsoidal iceball. Note the synergistic effect and the influence of the blood vessels and the saline solution that yield different iceball shape. This example illustrates the importance of a

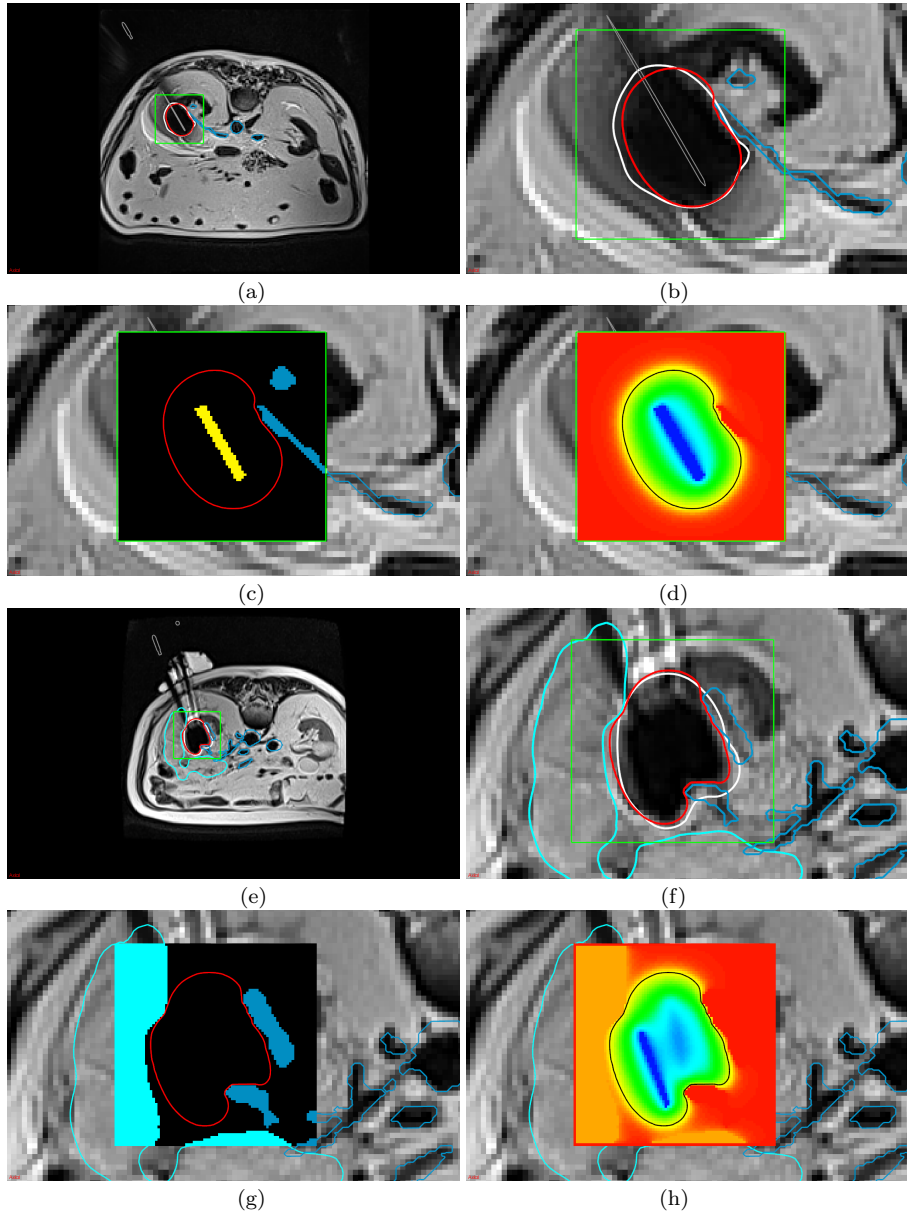


Fig. 4: Illustration of the simulation results at the end of the second freezing cycle of patient cases 2 (a-d) and 4 (e-h). In each group of 4 images, the top images (a,b and e,f respectively) show a representative intraoperative axial MRI slice (a and e full, b and f detail), with the 80 mm cube (green), the ground-truth iceball contour (white), the computed iceball contour (red), the blood vessels (dark blue) and the saline solution for case 4 (light blue). Images (c,g) show a detail of the same intraoperative axial MRI slice with the labels of the voxels inside the cube superimposed on them: freezing source (yellow), vessels and saline solution heating sources (blue) and iceball contour (red). Images (d,h) depict the temperature color map showing the 0°C iso-surface (black); blue is the minimum freezing temperature of -119.4°C and red is the maximum body temperature of 37°C .

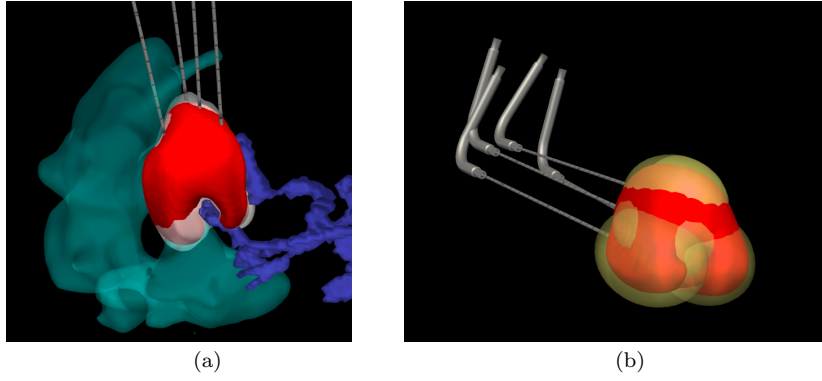


Fig. 5: 3D views of: (a) ground truth (white) and simulated (red) iceballs, four cryoprobes (gray), blood vessels (dark blue) and saline solution (light blue) after the first freezing cycle; (b) simulated iceball (red) and theoretical ellipsoids (yellow).

simulation based on an accurate simulation model rather than a theoretical one. The actual iceball differs significantly from theoretical ellipsoids and is smaller, which could lead to an insufficient ablation of the cancerous cells and a recurrence of the disease, or unexpected damages to surrounding structures.

Table 4 lists the Dice coefficients and the Hausdorff distances for the five patient cases and for the three cube sizes. These measurements indicate a close similarity between the two shapes, with an average Dice coefficient >0.79 in all cases. However, this comparison is subjected to the possible errors in the manual segmentation which can introduce inaccuracies.

We note that there is an additional phenomenon that reduces the accuracy of the simulated iceball. The interventions were all performed under MRI guidance using an MRI-compatible cryoprobe. The insulation of the cryoprobes is not sufficient to avoid a residual freezing along its body, resulting in an elongated shape along the cryoprobe, called by clinicians a “comet tail” (Fig. 6). When the freezing shaft is modeled as the only source of cold, without accounting for the residual cold along the body, the simulated iceball will not reproduce this comet tail, thereby leading to an inaccuracy of up to 10mm in the direction of the entry point. This explains why the Hausdorff distance may be >10 mm.

A second source of inaccuracy is that the simulations were performed considering that all cryoprobes were used at full power during the intervention. However, there are situations in which the interventional radiologist reduces the power of one or several cryoprobes to protect a particular structure. This indeed occurred in patient case 5, as illustrated in Fig. 5b. In this case, the ground truth and the simulated iceball shapes will exhibit a looser match, as the simulation is less faithful. However, note that in this case the upper boundary of the ground truth and simulated iceball fit tightly.

In terms of computation times, the results in Table 4 indicate that an 80mm cube yields comparable accuracy than those of a 100mm cube with a significantly shorter computation time: 22.85 secs vs. 76.82 secs on average. A 60mm cube yields results with a lower accuracy than those obtained with the 80 and 100mm cubes with only a slight reduction of the computation times. However, since the

Table 4: Dice coefficient and Hausdorff distance (HD, in mm) measurements between the computed and the ground truth iceball segmentation shape at the end of the process (after the second freezing cycle).

Patient case	60mm			80mm			100mm		
	Dice	HD	Time	Dice	HD	Time	Dice	HD	Time
1	0.67	13.08	16.53	0.70	12.12	22.90	0.70	12.10	77.42
2	0.86	5.02	15.93	0.87	5.00	22.87	0.87	5.01	76.40
3	0.87	5.17	16.07	0.88	5.12	22.84	0.88	5.12	77.33
4	0.74	10.82	15.93	0.80	10.42	22.81	0.80	10.41	76.63
5	0.80	11.89	16.12	0.78	12.43	22.85	0.78	12.43	76.30
Mean	0.79	9.20	16.12	0.81	9.02	22.85	0.81	9.02	76.82

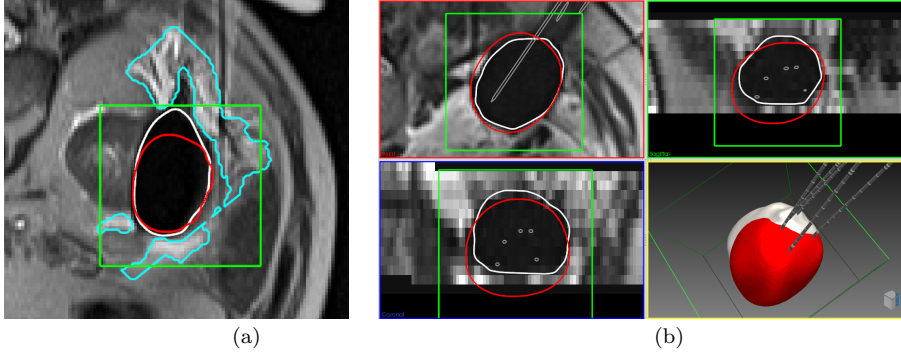


Fig. 6: (a) detail of an intraoperative axial MRI showing the “comet tail” effect in patient case 1. Superimposed are the cube (green), the ground-truth iceball contour (white), the computed iceball contour (red), and the saline solution (light blue); (b) detail of patient case 5 showing the two lower probes that were set to 60% of their freezing power.

difference in accuracy is sub-millimetric, it is an option to be considered to further reduce the computation time when needed. This of course depends on the number of cryoprobes used and the size of the resulting iceball that has to fit in such a small cube. In case of larger ablation volumes, larger cubes should be used.

Table 5 lists the computation times of the single-thread, multi-thread, and GPU variants of the algorithm, for the medium-sized cube of 80 mm. The results clearly show the advantage of the GPU computation. Note that the computation times do not depend on the complexity of the scene or on the number of heating structures. They only depend on the size of the cube and on the duration of the simulation process.

5 Conclusion

We have presented a new method for fast GPU-based iceball modeling based on the simulation of thermal propagation in the tissue based on the solution of the heat equation that accounts for the presence of heating sources around the iceball. Experimental results of two studies – an ex-vivo warm gel setup, and simulation

Table 5: Computation times (in seconds) for the single thread, multi-thread, and GPU implementations for a $80 \times 80 \times 80\text{mm}^3$ cube.

Patient case	Single thread	Multi-thread	GPU
1	361.986	152.056	22.904
2	446.945	169.855	22.870
3	449.754	161.105	22.843
4	374.193	151.726	22.809
5	451.389	162.521	22.846
Mean	416.853	159.453	22.854

on five retrospective patient cases of kidney tumors cryoablation with various levels of complexity of the vascular structure and warm saline solution around the tumor tissue – indicate that our method yields accurate iceball shape predictions. The accurate results and short computation times indicate that our method can be effectively incorporated in a comprehensive cryoablation preoperative planning system that optimizes the number and location of cryoprobes and that takes into account the presence of blood vessels and warm saline solution.

Directions of future work include comprehensive experimental studies on larger datasets, more elaborate in-vivo and ex-vivo experimental results for ground truth. The simulation model can be extended to account for the comet tail effect and for the inclusion of cryoprobes with various properties, types, and power delivery characteristics.

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Compliance with ethical standards

Conflict of interest: None of the authors has any conflict of interest. The authors have no personal financial or institutional interest in any of the materials, software or devices described in this article.

Protection of human and animal rights statement: No animals or humans were involved in this research. All images were anonymized before delivery to the researchers.

Presentation at conferences: This invited paper is a significantly expanded and detailed version of an accepted paper at the MICCAI 2018. The additions are a more detailed method section, a significantly augmented state of the art, four new experimental cases, and an augmented discussion.

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